

ALK-3

MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Jun 25 23:35:46 1997; MasPar time 2402.20 Seconds

Tabular output not generated.

Title: >US-08-436-265-5

Description: (1-2932) from US08436265.seq

Perfect Score: 2932

N.A. Sequence: 1 GCTCCGCGCGAGGGCTGGA.....GCTTATTGCAATCACCC 2932

Comp: CGAGGCGGCTCCGACCT.....CGAATAACGTTTAGTCGG

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 333249 seqs, 555961234 bases x 2

Processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-new11

1: BCT 2: FUN 3: GEN 4: HUM1 5: HUM2 6: HUM3 7: INV1 8: INV2

9: INV3 10: INV4 11: INV5 12: INV6 13: INV7 14: ORG 15: MAM

16: VRT 17: PLN 18: PRO1 19: PRO2 20: ROD 21: SYN 22: UNC

23: VIR1 24: VIR2

Database: genbank97

25: BCT1 26: BCT2 27: BCT3 28: BCT4 29: BCT5 30: BCT6 31: BCT7

32: BCT8 33: BCT9 34: GEN1 35: GEN2 36: HTG 37: INV1 38: INV2

39: INV3 40: INV4 41: INV5 42: INV6 43: INV7 44: INV8 45: INV9

46: MAM1 47: MAM2 48: MAM3 49: VRT1 50: VRT2 51: VRT3 52: PAT1

53: PAT2 54: PAT3 55: PAT4 56: PHG 57: PLN1 58: PLN2 59: PLN3

60: PLN4 61: PLN5 62: PLN6 63: PLN7 64: PLN8 65: PLN9 66: PLN10

67: PRI1 68: PRI2 69: PRI3 70: PRI4 71: PRI5 72: PRI6 73: PRI7

74: PRI8 75: PRI9 76: PRI10 77: PRI11 78: PRI12 79: PRI13

80: PRI14 81: ROD1 82: ROD2 83: ROD3 84: ROD4 85: ROD5 86: ROD6

87: ROD7 88: ROD8 89: STR 90: SYN 91: UNA 92: VRL1 93: VRL2

94: VRL3 95: VRL4 96: VRL5 97: VRL6 98: VRL7 99: VRL8 100: VRL9

Database: genbank-new11

101: BCT 102: GEN 103: INV1 104: INV2 105: MAM 106: VRT

107: PHG 108: PLN 109: PRI1 110: PRI2 111: ROD 112: SYN

113: UNA 114: VRL

Database: u-emb148_97

115: part1 116: part2

Statistics: Mean 12.320; Variance 4.881; scale 2.524

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description Pred. No.
1	2932	100.0	2932 70 HSALK3A H.sapiens ALK-3 mRNA. 0.00e+00
2	1408	48.0	3167 88 S75359 bone morphogenetic pr 0.00e+00
3	1403	47.9	2292 84 MUSBMPRC Mouse mRNA for BMP re 0.00e+00
4	1380	47.1	2402 82 MMU04672 Mus musculus type I r 0.00e+00
5	1334	45.5	2620 20 S74037 bone morphogenetic pr 0.00e+00
6	1334	45.5	3003 87 RATRALK3 Rat mRNA for bone mor 0.00e+00
7	1334	45.5	3003 20 RNRALK3 Rat mRNA for bone mor 0.00e+00
8	1311	44.7	1599 81 MMALK3A M.musculus ALK-3 mRNA 0.00e+00
9	1275	43.5	1599 87 RATR94R1 Rat mRNA for bone mer 0.00e+00
10	1223	41.7	2056 82 MMU04673 Mus musculus NIH3T3 t 0.00e+00
11	967	33.0	1969 49 CHKRK1R Gallus gallus (clones 0.00e+00

12 671 22.9 2315 51 XLU16654 Xenopus laevis BMP re 0.00e+00

13 508 17.3 1944 81 MMALK6A M.musculus ALK-6 mRNA 0.00e+00

14 489 16.7 2252 49 CHKRPK1 Chicken mRNA for rece 0.00e+00

15 261 8.9 2308 75 HUMALK5A Human activin recepto 1.01e-228

RESULT 1

LOCUS HSALK3A 2932 bp RNA PRI 29-SEP-1993

DEFINITION H.sapiens ALK-3 mRNA.

ACCESSION Z22535

NID 9402186

KEYWORDS ALK-3 gene; cell surface receptor; serine threonine kinase.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; Mrochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2932)

AUTHORS ten Dijke,P., Ichijo,H.H., Franzen,P., Schulz,P., Saras,J.J., Toyoshima,H.H., Heldin,C.C. and Miyazono,K.K.

TITLE Activin receptor-like kinases; A novel subclass of cell surface receptors with predicted serine/threonine kinase activity

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2932)

AUTHORS ten Dijke,P.

TITLE Direct Submission

JOURNAL Submitted (Oct-1993) Peter P ten Dijke, Ludwig Institute for Cancer Research, Uppsala, branch, Biomedical Center, Husargatan 3, Uppsala, S-751 24, Sweden

REFERENCE 3 (bases 1 to 2932)

AUTHORS ten Dijke,P., Ichijo,H., Franzen,P., Schulz,P., Saras,J., Toyoshima,H., Heldin,C.H. and Miyazono,K.

TITLE Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity

JOURNAL Oncogene 8 (10), 2879-2887 (1993)

MEDLINE 93390967

Query Match 100.0%; Score 2932; DB 70; Length 2932;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 2932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

LOCUS S75359 3167 bp mRNA ROD 26-MAY-1995

DEFINITION bone morphogenetic protein type IA receptor [rats, 3167 nt].

ACCESSION S75359

NID 9834007

KEYWORDS rats.

SOURCE Rattus sp.

ORGANISM Rattus sp.

REFERENCE 1 (bases 1 to 3167)

AUTHORS Takeda,K.

TITLE Expression of serine/threonine kinase receptors during ectopic bone formation induced by bone morphogenetic protein (BMP)

JOURNAL Kokubyo Gakkai Zasshi 61 (4), 512-526 (1994)

MEDLINE 95204990

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 160455] from the original journal article. This sequence comes from Fig. 4.

Query Match 48.0%; Score 1408; DB 88; Length 3167;

Best Local Similarity 83.4%; Pred. No. 0.00e+00;

Matches 1944; Conservative 0; Mismatches 356; Indels 30; Gaps 22;

RESULT 3

LOCUS MUSBMPRC 2292 bp mRNA ROD 25-NOV-1994

DEFINITION Mouse mRNA for BMP receptor, complete cds.

ACCESSION D16250

NID 9577633

KEYWORDS BMP receptor.

SOURCE Mus musculus brain, library of K. Nakayama and M. Hosaka, cDNA to mRNA, clone mTR11-45.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 2292)
AUTHORS Suzuki,A., Thies,R.S., Yamaji,N., Song,J.J., Wozney,J., Murakami,K.
TITLE A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryo
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91, 10255-10259 (1994)
MEDLINE 95024092
COMMENT Submitted (13-MAY-1993) to DDBJ by:
Naoto Ueno
Faculty of Pharmaceutical Sciences
Sapporo, Hokkaido 060
Japan
Phone: 011-716-8513
Fax: 011-716-8513.

Query Match 47.9%; Score 1403; DB 84; Length 2292;
Best Local Similarity 88.2%; Pred. No. 0.00e+00;
Matches 1683; Conservative 0; Mismatches 214; Indels 11; Gaps 7;

DEFINITION MMU04672 2402 bp mRNA ROD 17-SEP-1994
ACCESSION U04672 Mus musculus type I receptor BRK-1 mRNA, complete cds.
NID 9538362
KEYWORDS BRK-1; bone morphogenetic protein receptor kinase-1; full-length receptor protein kinase.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.

REFERENCE 1 (bases 1 to 2402)
AUTHORS Koenig,B.B., Cook,J.S., Wolsing,D.H., Ting,J., Tiesman,J.P., Correa,P.B., Olson,C.A., Pecquet,A.L., Ventura,F., Grant,R.A., Chen,G., Wrana,J.L., Massague,J. and Rosenbaum,J.S.
TITLE Characterization and cloning of a putative receptor for BMP-2 and BMP-4 from NIH3T3 cells
JOURNAL Mol. Cell. Biol. 14, 5961-5974 (1994)
MEDLINE 94344106
REFERENCE 2 (bases 1 to 2402)
AUTHORS Rosenbaum,J.S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1993) Jan S. Rosenbaum, The Procter & Gamble Company, Miami Valley Laboratories, P.O. Box 398707, Cincinnati, OH 45239-8707, USA

Query Match 47.1%; Score 1380; DB 82; Length 2402;
Best Local Similarity 89.6%; Pred. No. 0.00e+00;
Matches 1596; Conservative 0; Mismatches 180; Indels 6; Gaps 5;
MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 00:16:31 1997; MasPar time 289.25 Seconds
Tabular output not generated.

Title: >US-08-436-265-5
Description: (1-2932) from US08436265.seq
Perfect Score: 2932
N.A. Sequence: 1 GCTCCGCGCGAGGGCTGGA.....GCTTTATTGCAATCACCC 2932
Comp: CGAGGCGCGCTCCGACCT.....CGAATAAACGTTTAGTGGG

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 121476 seqs, 46255616 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 10.052; Variance 5.698; scale 1.764

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Match	Length	ID	Description	Pred. No.
1	2932	100.0	2932	16 T06031	Human ALK-3 cDNA.	0.00e+00
2	2922	99.7	2932	11 Q66636	Human Activin recepto	0.00e+00
3	1419	48.4	2070	11 Q66640	Mouse Activin recepto	0.00e+00
4	1380	47.1	2402	14 Q90184	BRK-1 DNA.	0.00e+00
5	1380	47.1	2402	20 T27228	Bone morphogenetic pr	0.00e+00
6	1380	47.1	2402	23 T28021	Mouse BMP type I rece	0.00e+00
7	1296	44.2	1613	14 Q83530	Sequence encoding bon	0.00e+00
8	1223	41.7	2056	14 Q90183	Truncated BRK-1.	0.00e+00
9	578	19.7	706	23 T28027	Mouse incomplete BMP	0.00e+00
10	509	17.4	2076	14 Q83531	Sequence encoding bon	0.00e+00

RESULT 1
ID T06031 standard; cDNA; 2932 BP.
AC T06031;
DT 13-FEB-1996 (first entry)
DE Human ALK-3 cDNA.
KW ALK-3; OPI binding receptor; osteogenic protein 1; morphogenesis;
KW morphogen; agonist; antagonist; chimeric receptor; gene therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 310..1908
FT /*tag= a
FT sig_peptide 310..378
FT /*tag= b
FT mat_peptide 379..1905
FT /*tag= c
FT /product= human ALK-3
PN W09530003-A2.
PD 09-NOV-1995.
PF 28-APR-1995; U05467.
PR 29-APR-1994; US-236428.
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Dijke PT, Heldin C, Miyazano K, Sampath KT;
DR WPI; 95-393076/50.
DR P-PSDB; R85207.
PT Identifying osteogenic protein-1 receptor-binding analogue - useful
PT in the design of morphogen agonists and antagonists for therapeutic,
PT diagnostic and experimental purposes
PS Claim 1; Page 68-71; 95pp; English.
CC The Type-1 cell surface receptors ALK-2, ALK-3 and ALK-6 (given in
CC R85206, R85207 and R85209), encoded by cDNAs given in T06030-32,
CC respectively, have specific binding affinity for osteogenic
CC protein 1 (OPI) and OPI-related analogues. The cDNAs are used
CC to produce recombinant ALK-2, -3 and -6 in e.g. mammalian host
CC cells and to construct chimeric receptors that can modulate the
CC availability of OPI for receptor binding in vivo as a means of
CC gene therapy.
SQ Sequence 2932 BP; 849 A; 575 C; 643 G; 865 T;

Query Match 100.0%; Score 2932; DB 16; Length 2932;

Best Local Similarity 100.0%; Pred. No. 0.00e+00; Mismatches 2932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ID Q66636 standard; cDNA; 2932 BP.
AC Q66636;
DT 19-JAN-1995 (first entry)
DE Human Activin receptor-like kinase 3 (hALK-3) cDNA.

RESULT 3
ID Q66640 standard; cDNA; 2070 BP.

AC Q66640;
DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 3 (mALK-3) cDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.

RESULT 4
ID Q90184 standard; DNA; 2402 BP.

AC Q90184;
DT 01-NOV-1995 (first entry)
DE BRK-1 DNA.
KW BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein; ds.
OS Mus sp.

FT Key Location/Qualifiers
FT CDS 11..1609

FT /tag= a 11..79

FT sig_peptide 80..1606

FT mat_peptide 80..1606

FT /tag= c

FT *tag=

PN WC9514778-A.

PD 01-JUN-1995.

PF 23-NOV-1994; U13534.

PR 24-NOV-1993; US-158735.

PA (PROC) PROCTER & GAMBLE CO.

PI Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;

DR WPI; 95-206935/27.

DR P-PSDB; R74343.

PT New bone morphogenetic protein receptor kinase protein - used for

PT identifying cpds. capable of binding it and for developing therapeutic

PT cpds. and detection system(s)

PT Claim 3; Page 29-32; 49pp; English.

CC A cDNA library prepared from NIH3T3 poly-A RNA was screened with

CC J159 PCR fragment to isolate clone BRK-1 (sequence given in

CC Q90184) encoding full-length BMP receptor kinase protein (R74343).

CC Vectors including the DNA were used to express recombinant BRK-1 in

CC CHO and COS-7 hosts.

SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T;
Query Match 47.1%; Score 1380; DB 14; Length 2402;
Best Local Similarity 89.6%; Pred. No. 0.00e+00;
Matches 1596; Conservative 0; Mismatches 180; Indels 6; Gaps 5;
Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 00:21:54 1997; MasPar time 1832.45 Seconds
1025.705 Million cell updates/sec
Tabular output not generated.

Title: >US-08-436-265-5
Description: (1-2932) from US08436265.seq
Perfect Score: 2932
N.A. Sequence: 1 GCTCCGCGCGGAGGCTGGA.....GCTTTATTGCAATCACCC 2932
Comp: CGAGGCGCGGCTCCGACCT.....CGAATAACGTTAGTGG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 887282 seqs, 320523884 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	388	13.2	4G4	165	W39552	zc18g04.r1	Soares par	0.00e+00
2	355	12.1	357	65	HSC2ZA061	H. sapiens partial CD	0.00e+00	
c	3	286	9.8	292	217	W15390	zc18g04.s1	Soares par 0.00e+00
c	4	286	9.8	292	184	W15390	zc18g04.s1	Soares par 0.00e+00
5	283	9.7	423	57	H97091	yv89a08.r1	Homo sapie	0.00e+00
6	253	8.6	468	11	AA056911	EST379R Pig Spleen la	0.00e+00	
7	253	8.6	468	250	SSA56911	EST379R Pig Spleen la	0.00e+00	
8	250	8.5	263	116	N88732	K5301F Fetal heart, L	0.00e+00	
9	213	7.3	219	89	HUM213H12B	Human aorta cDNA 5'-e	0.00e+00	
10	204	7.0	211	61	HSC0HE101	H. sapiens partial CD	0.00e+00	

ALIGNMENTS
RESULT 1
LOCUS W39552 404 bp mRNA EST 10-OCT-1996
DEFINITION zc18g04.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
322710 5' similar to gb:222535_cds1 SERINE/THREONINE-PROTEIN KINASE
RECEPTOR R5 PRECURSOR (HUMAN) ;
RESULT 2
LOCUS HSC2ZA061 357 bp RNA EST 21-SEP-1995
DEFINITION H. sapiens partial cDNA sequence; clone c-22a06.
ACCESSION F11592
NID 9705894

RESULT 3
LOCUS W15390 292 bp mRNA EST 29-APR-1996
DEFINITION zc18g04.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
322710 3'.
ACCESSION W15390
NID g1289800
KEYWORDS EST.

RESULT 4
LOCUS W15390 292 bp mRNA EST 10-OCT-1996
DEFINITION zc18g04.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
322710 3'.
ACCESSION W15390
NID g1289800
KEYWORDS EST.

RESULT 5
LOCUS H97091 423 bp mRNA EST 11-DEC-1995
DEFINITION yv89a08.r1 Homo sapiens cDNA clone 249878 5'.
ACCESSION H97091
NID g1114134
KEYWORDS EST.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jun 24 17:49:57 1997; MasPar time 11.29 Seconds
513.505 Million cell updates/sec
Tabular output not generated.
Title: >US-08-436-265-6
Description: (1-532) from US08436265.pap
Perfect Score: 3981

Sequence: 1 MTOLYIVIRLLGAYLFIISR.....TALRIKKTTLAKMWESQDVKI 532

Scoring table: PAM 150
Gap 11

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq26

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 36.144; Variance 151.486; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	3981	100.0	532	14	R85207		Human ALK-3.	0.00e+00
2	3981	100.0	532	10	R55368		Human Activin recepto	0.00e+00
3	3915	98.3	532	19	R95225		Mouse BMP type I rece	0.00e+00
4	3915	98.3	532	13	R74343		BRK-1 protein.	0.00e+00
5	3915	98.3	532	17	R96201		Bone morphogenetic pr	0.00e+00
6	3900	98.0	532	13	R70237		Bone morphogenic prot	0.00e+00
7	3615	90.8	500	13	R74342		Truncated BRK-1.	0.00e+00
8	2757	69.3	502	14	R85209		Mouse ALK-6.	3.26e-264
9	2757	69.3	502	13	R70238		Bone morphogenic prot	3.26e-264
10	2747	69.0	502	19	R95236		Chick BMP type I rece	3.45e-263

ALIGNMENTS

RESULT 1
ID R85207 standard; Protein; 532 AA.

AC R85207;
DT 13-FEB-1996 (first entry)
DE Human ALK-3.
KW ALK-3; OPI binding receptor; osteogenic protein 1; morphogenesis;
KW morphogen; agonist; antagonist.
OS Homo sapiens.

FT Key Location/Qualifiers

FT Peptide 1..23
FT /label= Sig_peptide
FT Domain 24..152
FT /label= Extracellular domain
FT Domain 153..235
FT /label= Transmembrane domain
FT Domain 236..527
FT /label= Intracellular domain
FT /note= "serine/threonine-kinase domain"

PN W09530003-A2.

PD 09-NOV-1995.

PF 28-APR-1995; U05467.

PR 29-APR-1994; US-236428.

PA (CREA-) CREATIVE BIOMOLECULES INC.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Dijke PT, Heidin C, Miyazano K, Sampath KT;

DR WPI: 95-393076/50.

DR N-PSDB; T06031.

PT Identifying osteogenic protein-1 receptor-binding analogue - useful in the design of morphogen agonists and antagonists for therapeutic, diagnostic and experimental purposes

PS Claim 1; Page 68-71; 95pp; English.

CC The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (given in

CC R85206, R85207 and R85209 have specific binding affinity for osteogenic protein 1 (OP1) and OP1-related analogues. The receptors are used to identify novel morphogen receptor binding analogues useful in drug design.

SQ Sequence 532 AA;

Query Match 100.0%; Score 3981; DB 14; Length 532;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

ID R55368 standard; Protein; 532 AA.

AC R55368;

DT 20-JAN-1995 (first entry)

DE Human Activin receptor-like kinase 3 (hALK-3).

KW serine threonine kinases; activin receptors; Act-R; superfamily;

KW transforming growth factor; TGF; diagnostics; detection; therapy;

KW rheumatoid arthritis; glomerular nephritis; fibrosis.

OS Homo sapiens.

PN W09411502-A.

PD 26-MAY-1994.

PF 17-NOV-1993; G02367.

PR 17-NOV-1992; GB-024057.

PR 08-MAR-1993; GB-004677.

PR 08-MAR-1993; GB-004677.

PR 28-MAY-1993; GB-011047.

PR 02-JUL-1993; GB-013763.

PR 03-AUG-1993; GB-016099.

PR 15-OCT-1993; GB-021344.

PA (LUDW-) LUDWIG INST CANCER RES.

RESULT 3

ID R95225 standard; Protein; 532 AA.

AC R95225;

DT 31-DEC-1996 (first entry)

DE Mouse BMP type I receptor kinase protein (BRK-1).

KW BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;

KW BMP type I receptor kinase; BRK-1; BMP receptor.

OS Mus sp.

PN W09614579-A1.

PD 17-MAY-1996.

PF 30-OCT-1995; U14027.

PR 04-NOV-1994; US-334178.

PR 05-JUN-1995; US-462467.

PA (PROC) PROCTER & GAMBLE CO.

RESULT 4

ID R74343 standard; Protein; 532 AA.

AC R74343;

DT 01-NOV-1995 (first entry)

DE BRK-1 protein.

KW BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein.

OS Mus sp.

PH Key Location/Qualifiers

FT Peptide 1..23

FT /label= Sig_peptide

FT Domain 24..152

FT /label= Extracellular ligand_binding_domain

FT Domain 153..176

FT /label= Transmembrane domain

FT Domain 177..532

FT /label= Intracellular_kinase_domain

PN W09514778-A.

PD 01-JUN-1995.

PF 23-NOV-1994; U13534.

PR 24-NOV-1993; US-158735.

PA (PROC) PROCTER & GAMBLE CO.

PI Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;

Query Match 98.3%; Score 3915; DB 13; Length 532;

Best Local Similarity 98.1%; Pred. No. 0.00e+00;

Matches 522; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

RESULT 5

ID R96201 standard; Protein; 532 AA.

AC R96201;

DT 22-FEB-1996 (first entry)

DE Bone morphogenetic protein type-I receptor kinase-1.

KW Mouse; bone morphogenetic protein receptor kinase-1;

KW bone morphogenetic protein receptor kinase-3; antibody; diagnostic;

KW bone disorder; osteogenic; bone morphogenetic protein-agonist;

KW drug screening; reporter gene; bone morphogenetic protein-antagonist;

KW hormone-responsive element.

OS Mus musculus.

FH Key Location/Qualifiers

FT Peptide 216..221

FT /note= "Conserved BRK-1 motif"

FT Peptide 398..421

FT /note= "Peptide used to raise antibody"

PN W09614412-A2.

PD 17-MAY-1996.

PF 30-OCT-1995; U14085.

PR 04-NOV-1994; US-334179.

PA (PROC) PROCTER & GAMBLE CO.

PI Mohno T, Rosenbaum JS;

RESULT 6

ID R70237 standard; Protein; 532 AA.

AC R70237;

DT 28-SEP-1995 (first entry)

DE Bone morphogenetic protein receptor CFK1-23a.

KW Bone morphogenetic protein, receptor; serine/threonine kinase; BMP;

KW bone; cartilage; injury; treatment; inhibition.

OS Rattus rattus.

PN W09507982-A.

PD 23-MAR-1995.

PF 07-SEP-1994; U10080.

PR 17-SEP-1993; US-123934.

PA (GEMY) GENETICS INST INC.

PI Celeste AJ, Thies RS, Wozney JM, Yamaji N, A;

Query Match 98.0%; Score 3900; DB 13; Length 532;

Best Local Similarity 97.2%; Pred. No. 0.00e+00;

Matches 517; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

|||||||

OY 481 PIVSNRWNSDE 491

RESULT 8

ID R85209 standard; Protein; 502 AA.

AC R85209;

DT 13-FEB-1996 (first entry)

DE Mouse ALK-6.

KW ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis;

KW morphogen; agonist; antagonist.

OS Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..22

FT /label= Sig_peptide

FT Domain 23..122

FT /label= Extracellular domain

FT Domain 123..205

FT /label= Transmembrane domain

FT Domain 206..497

FT /label= Intracellular domain

FT /note= "serine/threonine-kinase domain"

PN W09530003-A2.

PD 09-NOV-1995.

PF 28-APR-1995; U05467.

PR 29-APR-1994; US-236428.

PA (CREA-) CREATIVE BIOMOLECULES INC.

PA (LUDW-) LUDWIG INST CANCER RES.

PI DiJke PT, Heldin C, Miyazano K, Sampath KT;

DR WPI; 95-393076/50.

DR N-PSDB; T06032.

PT Identifying osteogenic protein-1 receptor-binding analogue - useful in the design of morphogen agonists and antagonists for therapeutic, diagnostic and experimental purposes

PS Claim 1; Page 73-76; 95pp; English.

CC The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (given in R85206, R85207 and R85209) have specific binding affinity for osteogenic protein 1 (OP1) and OP1-related analogues. The receptors are used to identify novel morphogen receptor binding analogues useful in drug design.

SQ Sequence 502 AA;

Query Match 69.3%; Score 2757; DB 14; Length 502;

Best Local Similarity 71.9%; Pred. No. 3.26e-264;

Matches 363; Conservative 76; Mismatches 61; Indels 5; Gaps 5;

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jun 24 17:48:18 1997; MasPar time 19.20 Seconds

789.840 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-6

Description: (1-532) from US08436265.pep

Perfect Score: 3981

Sequence: 1 MTQLYIYIRLLGAYLFISR.....TALRIKKTAKWVESQDYKI 532

Scoring table: PAM 150

Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir50

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3

8:unann4 9:unann5 10:unann6 11:unann7 12:unann8

13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 49.071; Variance 114.924; scale 0.427

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	3981	100.0	532	13	S37183	ALK-3 protein - huma	0.00e+00
2	3981	100.0	532	13	I37163	ALK-3 - human	0.00e+00
3	3915	98.3	532	14	A56238	bone morphogenetic p	0.00e+00
4	3900	98.0	532	14	JC2387	bone morphogenetic p	0.00e+00
5	3615	90.8	500	14	B56238	bone morphogenetic p	0.00e+00
6	3139	78.8	527	12	A54985	BMP receptor precurs	0.00e+00
7	2757	69.3	502	14	A53444	activin receptor-lik	0.00e+00
8	2757	69.3	502	14	JC2491	serine/threonine kin	0.00e+00
9	2747	69.0	502	13	A56683	receptor protein kin	0.00e+00
10	1762	44.3	503	13	A49432	activin receptor-lik	1.95e-283

RESULT 3

ENTRY A56238 #type complete

TITLE bone morphogenetic protein receptor BRK-1 - mouse

ALTERNATE_NAMES ALK-3 protein; BMP receptor

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 06-Sep-1996

QY	121	TIECRTLNCNOYLQPTLPVVGFFDGSIRVLVLLISMAVCIAMIFSSCFCKHYC	180
Db	181	ksisrgrnyrdleqdeafipvgesklldidqsgsgsgpllvqvtiakqigmrvq	240
QY	181	KSISRRRRYRDLEQDEAFIPVGESLKDLDQSSQSGSGPLLVQRTIAQIQMVQV	240
Db	241	gkgrgygevwmkgwrgekavkvffteeaswffreteiyqvtlmrhenilgfiaadikgtg	300
QY	241	GKGRYGEVWMKGWRGEKAVKVFFTTEASWFFRETEIYQVTLMRHENILGFIAADIKGTG	300
Db	301	swtdlyltdyhengslydflikcatldtralliklaysaacglchlhteiygtcgkpaiah	360
QY	301	SWTQLYLI TDYHENGSLYDFLIKCATLDTRALLKLAYSAAACGLCHLHTEIYGTGQKPAIAH	360
Db	361	rdlksknllikkngscciajiglavkfnsdtnedplntrvgtkrymapevldeslkn	420
QY	361	RDLSKNLLIKKNGSCCIADJGLAVKFNSDTEVDPLNTRVGTKRYMAPEVLDLSLKN	420
Db	421	hfqpyimadiysfgliiwemarrcitgtgiveeqlypynnmpsdpsyedmrevvcvkrlr	480
QY	421	HFQPYIMADIYSFGLIIWEMARRCITGTGIVEEQLYPYNNMVPSPDSYEDMREVVCVKRLR	480
Db	481	pivsnrwnsdeclravlkmscawahnpasrItalrikktlaknvesqdski	532
QY	481	PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKNVESQDVKI	532
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm			
Run on:	Tue Jun 24 17:46:53 1997;	MaSPar time 13.15 Seconds	
Tabular output not generated.		858.137 Million cell updates/sec	
Title:	>US-08-436-265-6		
Description:	(1-532) from US08436265.pep		
Perfect Score:	3981		
Sequence:	1 MTQLYLYIKLLGAYLFIISR.....TALRIKKTAKNVESQDVKI 532		
Scoring table:	PAM 150		
	Gap 11		
Searched:	59021 seqs, 21210388 residues		
Post-processing:	Minimum Match 0%		
	Listing first 45 summaries		
Database:	swiss-prot34		
	1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7		
	8:part8 9:part9 10:part10 11:part11		
Statistics:	Mean 50.780;	Variance 83.714;	scale 0.607
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Match Length DB	ID Description Pred. No.
1	3981	100.0	532 5 KIR5 HUMAN SERINE/THREONINE-PROT 0.00e+00
2	3915	98.3	532 5 KIR5 MOUSE SERINE/THREONINE-PROT 0.00e+00
3	2757	69.3	502 5 KIR6_MOUSE SERINE/THREONINE-PROT 0.00e+00
4	2747	69.0	502 5 KIR6_CHICK SERINE/THREONINE-PROT 0.00e+00
5	1762	44.3	503 5 KIR4 HUMAN SERINE/THREONINE-PROT 0.00e+00
6	1737	43.6	501 5 KIR4_FAT SERINE/THREONINE-PROT 0.00e+00
7	1638	41.1	509 5 KIR1 RAT SERINE/THREONINE-PROT 0.00e+00
8	1630	40.9	509 5 KIR1 HUMAN SERINE/THREONINE-PROT 0.00e+00
9	1617	40.6	509 5 KIR1_MOUSE SERINE/THREONINE-PROT 0.00e+00
10	1614	40.5	505 5 KIR2 HUMAN SERINE/THREONINE-PROT 0.00e+00

Scoring table: TABLE default
Gap 6

Mismatch STD : Dbase 0; Query 0

Searched: 53119 seqs, 14293498 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: 1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93
10:PCT94 11:PCT95 12:PCT96

Statistics: Mean 9.515; Variance 4.793; scale 1.985

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2932	100.0	2932	11	PCT-US95-0	Sequence 5, Applicatio	0.00e+00
2	1296	44.2	1813	10	PCT-US94-1	Sequence 1, Applicatio	0.00e+00
3	509	17.4	2076	10	PCT-US94-1	Sequence 3, Applicatio	0.00e+00
4	508	17.3	1952	11	PCT-US95-0	Sequence 7, Applicatio	0.00e+00
5	255	8.7	1506	5	US-08-149-	Sequence 2, Applicatio	8.06e-183
6	255	8.7	1506	5	US-08-317-	Sequence 2, Applicatio	8.06e-183
7	252	8.6	1647	10	PCT-US94-1	Sequence 7, Applicatio	2.52e-180
8	244	8.3	3238	10	PCT-US94-1	Sequence 5, Applicatio	1.12e-173
9	241	8.2	1506	5	US-08-149-	Sequence 4, Applicatio	3.45e-171
10	241	8.2	1506	5	US-08-317-	Sequence 4, Applicatio	3.45e-171

ALIGNMENTS

RESULT 1
ID PCT-US95-05467-5 STANDARD; DNA; UNC; 2932 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 5, Application PC/TUS9505467.
CC Sequence 5, Application PC/TUS9505467
CC GENERAL INFORMATION:
CC APPLICANT:
CC APPLICANT:
CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL
CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR
CC NUMBER OF SEQUENCES: 15
MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 14:32:34 1997; MasPar time 5.02 Seconds
348.411 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-6
Description: (1-532) from US08436265.pep
Perfect Score: 3981
Sequence: 1 MTQLYIVIRLLGAYLFIISR.....TALRIKTKLAKWVESQDVKI 532

Scoring table: PAM 150
Gap 11

Searched: 35845 seqs, 3290575 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93
10:PCT94 11:PCT95 12:PCT96

Statistics: Mean 34.082; Variance 164.028; scale 0.208

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	3981	100.0	532	11	PCT-US95-0	Sequence 6, Applicatio	0.00e+00
2	3900	98.0	532	10	PCT-US94-1	Sequence 2, Applicatio	0.00e+00
3	2757	69.3	502	10	PCT-US94-1	Sequence 4, Applicatio	4.14e-231
4	2757	69.3	502	11	PCT-US95-0	Sequence 8, Applicatio	4.14e-231
5	1754	44.1	503	10	PCT-US94-1	Sequence 10, Applicati	8.61e-142
6	1737	43.6	501	5	US-08-149-	Sequence 17, Applicati	2.78e-140
7	1737	43.6	501	5	US-08-317-	Sequence 17, Applicati	2.78e-140
8	1638	41.1	509	10	PCT-US94-1	Sequence 6, Applicatio	1.67e-131
9	1630	40.9	509	11	PCT-US95-0	Sequence 4, Applicatio	8.54e-131
10	1625	40.8	509	5	US-08-149-	Sequence 14, Applicati	2.37e-130

ALIGNMENTS

RESULT 1
ID PCT-US95-05467-6 STANDARD; PRT; 532 AA.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 6, Application PC/TUS9505467.
CC Sequence 6, Application PC/TUS9505467
CC GENERAL INFORMATION:
CC APPLICANT:
CC APPLICANT:
CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL
CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR

RESULT 2
ID PCT-US94-10080-2 STANDARD; PRT; 532 AA.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 2, Application PC/TUS9410080.
CC Sequence 2, Application PC/TUS9410080
CC GENERAL INFORMATION:
CC APPLICANT: GENETICS INSTITUTE, INC.
CC TITLE OF INVENTION: RECEPTOR PROTEINS
CC NUMBER OF SEQUENCES: 19
Query Match 98.0%; Score 3900; DB 10; Length 532;
Best Local Similarity 97.2%; Pred. No. 0.00e+00;
Matches 517; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 00:53:14 1997; MasPar time 1709.29 Seconds
1346.573 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-13
Description: (1-2070) from US08436265.seq
Perfect Score: 2070
N.A. Sequence: 1 ATTTCATGAGATGGAGACATA.....TTTCCTTTTITGTTTGT 2070
Comp: TAAGTACTCTACCTTCGTAT.....AACGAAAAAACAAACAA

Scoring table: TABLE default

Searched: 333249 seqs, 555961234 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new11
1-BCT 2:FUN 3:GEN 4:HUM1 5:HUM2 6:HUM3 7:INV1 8:INV2
9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM
16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
23:VIR1 24:VIR2

Database: genbank97
25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7
32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2
39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9
46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1
53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3
60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10
67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7
74:PRI8 75:PRI9 76:PRI10 77:PRI11 78:PRI12 79:PRI13
80:PRI14 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6
87:ROD7 88:ROD8 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2
94:VRL3 95:VRL4 96:VRL5 97:VRL6 98:VRL7 99:VRL8 100:VRL9

Database: Genbank-new11
101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT
107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN
113:UNA 114:VRL
Database: u-emb148_97
115:part1 116:part2

Statistics: Mean 12.028; Variance 5.236; scale 2.297
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.	LOCUS DEFINITION	Accession	RNA
1	1973	95.3	2292	84	MUSEMPRC	Mouse mRNA for BMP re	0.00e+00	MMALK3A	1599 bp
2	1795	86.7	2402	82	MMU04672	Mus musculus type I r	0.00e+00	Z23154	M.musculus ALK-3 mRNA, complete CDS.
3	1665	80.4	2056	82	MMU04673	Mus musculus NIH3T3 t	0.00e+00		
4	1647	79.6	3167	88	S75359	bone morphogenetic pr	0.00e+00		
5	1599	77.2	1599	81	MMALK3A	M.musculus ALK-3 mRNA	0.00e+00	g437868	ALK-3 gene; serine/threonine kinase receptor.
6	1564	75.6	2620	20	S74037	bone morphogenetic pr	0.00e+00		
7	1564	75.6	3003	87	RATRALK3	Rat mRNA for bone mor	0.00e+00		
8	1564	75.6	3003	20	RNRALK3	Rat mRNA for bone mor	0.00e+00		
9	1457	70.4	1599	87	RATRB4R1	Rat mRNA for bone mer	0.00e+00		
10	1417	68.5	2932	70	HSALK3A	H.sapiens ALK-3 mRNA.	0.00e+00		
RESULTS									
LOCUS	MUSEMPRC		2292 bp		mRNA		ROD		25-NOV-1994
DEFINITION	Mouse mRNA for BMP receptor, complete cds.								
ACCESSION	D16250								
NID	9577633								
KEYWORDS	BMP receptor.								
SOURCE	Mus musculus brain, library of K. Nakayama and M. Hosaka, cDNA to mRNA, clone mTFR11-45.								
ORGANISM	Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.								
REFERENCE	1 (bases 1 to 2292)								
AUTHORS	Suzuki, A., Thies, R.S., Yamaji, N., Song, J.J., Wozney, J., Murakami, K. and Kung, H.								
TITLE	A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryo								
RESULT ID	6		S74037		backbone; RNA; ROD; 2620 BP.				

AC S74037; D38082;
NI 9765229
DT 26-AUG-1996 (Rel. 49, Created)
DT 26-AUG-1996 (Rel. 49, Last updated, Version 1)
DE bone morphogenetic protein type IA receptor [rats, Wistar, dental
DE pulp cell line RPC-C2A, mRNA, 2620 nt].
KW .
OS Rattus sp. (rat)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-2620
RX MEDLINE; 95032096.
RA Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T.,
RA Sasaki S.;
RT "Molecular cloning of rat bone morphogenetic protein (BMP) type IA
RT receptor and its expression during ectopic bone formation induced
RT by BMP";
RL Biochem. Biophys. Res. Commun. 204:203-209(1994) .

RESULT 8
ID RNRALK3 standard; RNA; ROD; 3003 BP.
AC D38082;
EX gl398909
DT 01-DEC-1994 (Rel. 42, Created)
DT 08-SEP-1996 (Rel. 49, Last updated, Version 3)
DE Rat mRNA for bone morphogenetic protein type IA receptor, complete
DE cds.
KW BMP receptor; bone; bone morphogenetic protein type IA receptor;
KW kinase; morphogenetic protein receptor; rALK-3; serine/threonine;
KW transmembrane protein.
OS Rattus norvegicus (rat)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-3003
RA Oida S.;
RA Oida S.;
RT ;
RL Submitted (26-AUG-1994) to the EMBL/GenBank/DBJ databases.
RL Shinichi Oida, Faculty of Dent., Tokyo Medical and Dental
RL University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku,
RL Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)
RN [2]
RP 1-3003
RX MEDLINE; 95032096.
RA Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T.,
RA Sasaki S.;
RT "Molecular cloning of rat bone morphogenetic protein (BMP) type IA
RT receptor and its expression during ectopic bone formation induced
RT by BMP";
RL Biochem. Biophys. Res. Commun. 204:203-209(1994) .

Query Match 75.6%; Score 1564; DB 20; Length 3003;
Best Local Similarity 93.9%; Pred. No. 0.00e+00;
Matches 1727; Conservative 0; Mismatches 103; Indels 10; Gaps 5;

RESULT 10
LOCUS HSALK3A 2932 bp RNA PRI 29-SEP-1993
DEFINITION H.sapiens ALK-3 mRNA.
ACCESSION Z22535
NID 9402186
KEYWORDS ALK-3 gene; cell surface receptor; serine threonine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2932)
AUTHORS ten Dijke, P., Ichijo, H., Franzen, P., Schulz, P., Saras, J.,
Toyoshima, H., Heldin, C.C. and Miyazono, K.
TITLE Activin receptor-like kinases: A novel subclass of cell surface
receptors with predicted serine/threonine kinase activity

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2932)
AUTHORS ten Dijke, P.
TITLE Direct Submission
JOURNAL Submitted (06-APR-1993) Peter P ten Dijke, Ludwig Institute for
Cancer Research, Uppsala, branch, Biomedical Center, Husargatan 3,
Uppsala, S-751 24, Sweden
REFERENCE 3 (bases 1 to 2932)
AUTHORS ten Dijke, P., Ichijo, H., Franzen, P., Schulz, P., Saras, J.,
Toyoshima, H., Heldin, C.H. and Miyazono, K.
TITLE Activin receptor-like kinases: a novel subclass of cell-surface
receptors with predicted serine/threonine kinase activity
Oncogene 8 (10), 2879-2887 (1993)
JOURNAL 93390967
MEDLINE
MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 01:22:24 1997; MasPar time 199.07 Seconds
Tabular output not generated. 961.959 Million cell updates/sec

Title: >US-08-436-265-13
Description: (1-2070) from US08436265.seq
Perfect Score: 2070
N.A. Sequence: 1 ATTCATGAGATGGAACATA.....TTTGCTTTTGTGTTTGT 2070
Comp: TAAGTACTTACTCTCGTAT.....AAACGAAAAACAAACAA

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 121476 seqs, 46255616 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: n-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 9.797; Variance 5.887; scale 1.664

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	2066	99.8	2070	11	Q66640	Mouse Activin recepto	0.00e+00	0.00e+00
2	1795	86.7	2402	23	T28021	Mouse BMP type I rece	0.00e+00	0.00e+00
3	1795	86.7	2402	20	T27228	Bone morphogenetic pr	0.00e+00	0.00e+00
4	1795	86.7	2402	14	Q90184	BRK-1 DNA.	0.00e+00	0.00e+00
5	1665	80.4	2056	14	Q90183	Truncated BRK-1.	0.00e+00	0.00e+00
6	1538	74.3	1813	14	Q83530	Sequence encoding bon	0.00e+00	0.00e+00
7	1417	68.5	2932	16	T06031	Human ALK-3 cDNA.	0.00e+00	0.00e+00
8	1411	68.2	2932	11	Q66636	Human Activin recepto	0.00e+00	0.00e+00
9	702	33.9	706	23	T28027	Mouse incomplete BMP	0.00e+00	0.00e+00
10	593	28.6	635	22	T33870	Modified bone morphog	0.00e+00	0.00e+00

ALIGNMENTS

RESULT 1
ID Q66640 standard; cDNA; 2070 BP.
AC Q66640;
DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 3 (mALK-3) cDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;

transforming growth factor; TGF; diagnostics; detection; therapy;
rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
Mus musculus.
Key Location/Qualifiers
5'UTR 1..216
/*tag= a
CDS 217..1815
/*tag= b
/*tag= c
/product= activin receptor-like kinase 3
3'UTR 1816..2070
/*tag= c
WO9411502-A.
26-MAY-1994.
17-NOV-1993; G02367.
17-NOV-1992; GB-024057.
08-MAR-1993; GB-004677.
08-MAR-1993; GB-004680.
28-MAY-1993; GB-011047.
02-JUL-1993; GB-013763.
03-AUG-1993; GB-016099.
15-OCT-1993; GB-021344.
(LUDW-) LUDWIG INST CANCER RES.
Dijke P, Franzen P, Heidin C, Miyazono K, Yamashita H;
WPI; 94-183503/22.
2041 GGTATTGTTGCTTTTGTGTTTGT 2070

RESULT 2
ID T28021 standard; cDNA; 2402 BP.
AC T28021;
DT 31-DEC-1996 (first entry)
DE Mouse BMP type I receptor kinase (BRK-1) cDNA.
KW BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
BMP type I receptor kinase; BRK-1; BMP receptor; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 11..1609
/*tag= e
WO9614579-A1.
17-MAY-1996.
30-OCT-1995; U14027.
04-NOV-1994; US-334178.
05-JUN-1995; US-462467.
(PROC) PROCTER & GAMBLE CO.
PI Rosenbaum JS;
DR WPI; 96-251887/25.
P-PSDB; R95225.
Assays for bone morphogenetic protein activities - using complex of
BMP type I receptor kinase protein and BMP receptor kinase protein
BRK-3
Claim 5; Page 64-66; 101pp; English.
CC A cDNA clone (T28021) codes for full-length mouse bone morphogenetic
protein (BMP) type I receptor kinase protein-1 (BRK-1) (R95225), a
receptor capable of binding BMP and transducing a signal initiated
by the binding. Host cells co-transfected with vectors carrying
full-length, incomplete or soluble BMP type I receptor kinase
protein cDNA and full-length, incomplete, soluble or truncated
BMP type II receptor kinase protein-3 (BRK-3) cDNA (see also
T28018-20 and T28022-30) express a BMP receptor complex useful for
screening cpds. for BMP receptor affinity or for determining the
concentration of a BMP receptor ligand in a clinical sample.
SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T;

Query Match 86.7%; Score 1795; DB 23; Length 2402;
Best Local Similarity 99.3%; Pred. No. 0.00e+00;
Matches 1859; Conservative 0; Mismatches 4; Indels 10; Gaps 4;

RESULT 3
ID T27228 standard; cDNA; 2402 BP.
AC T27228;

22-AUG-1996 (first entry)
Bone morphogenetic protein type-I receptor kinase-1 gene.
Mouse; bone morphogenetic protein receptor kinase-1;
bone morphogenetic protein receptor kinase-3; antibody; diagnostic;
bone disorder; osteogenic; bone morphogenetic protein-agonist;
drug screening; reporter gene; bone morphogenetic protein-antagonist;
hormone-responsive element; ds.
Mus musculus.
Key Location/Qualifiers
CDS 11..1609
/*tag= a
/product= Bone morphogenetic protein receptor kinase-1
WO9614412-A2.
17-MAY-1996.
30-OCT-1995; U14085.
04-NOV-1994; US-334179.
(PROC) PROCTER & GAMBLE CO.
PI Nohno T, Rosenbaum JS;
DR WPI; 96-251762/25.
P-PSDB; R96201.
isolated bone morphogenic protein receptor kinase protein - used to
determine if a test cpd. is capable of binding to, or is
(ant)agonist of BMP receptor kinase protein transcription
Example 4; Page 61-63; 87pp; English.
CC The sequence encodes mouse bone morphogenetic protein (BMP)
receptor type-I kinase-1 (BRK-1), which induces cellular
differentiation in response to BMP. The gene may be inserted in
plasmid pJT4, to form plasmid pJT4-J159F, and co-expressed with a
type-II BRK-3 gene to study complex formation between the 2
receptor types. The BRK-3 receptor and antibodies against it may
be used in diagnostic assays for BMP disorders, or in therapy to
bind or scavenge BMPs. In addition, expression of the BRK-3 gene
along with a reporter gene under the control of a hormone-
responsive element in a cell culture may be used to screen
compounds for BRK-agonist or -antagonist activity, by monitoring
reporter gene expression.
SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T;

Query Match 86.7%; Score 1795; DB 20; Length 2402;
Best Local Similarity 99.3%; Pred. No. 0.00e+00;
Matches 1859; Conservative 0; Mismatches 4; Indels 10; Gaps 4;

RESULT 6
ID Q83530 standard; DNA; 1813 BP.
AC Q83530;
DT 28-SEP-1995 (first entry)
DE Sequence encoding bone morphogenic protein receptor CPK1-23a.
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
bone; cartilage; injury; treatment; inhibition; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 61..1659
/*tag= a
/product= Bone morphogenic protein receptor.
WO9507982-A.
23-MAR-1995.
07-SEP-1994; U10080.
17-SEP-1993; US-123934.
(GEMY) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
P-PSDB; R70237.
Truncated BMP and serine/threonine kinase receptor proteins -
used to inhibit the effects of BMP-2 and/or BMP-4.
Claim 2; Page 48-50; 83pp; English.
CC Truncated bone morphogenic protein (BMP) receptors and
serine/threonine kinase receptors may be used in compositions to
inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
receptors pref. comprise the ligand binding domain, but not the
serine/threonine kinase and transmembrane domains. The truncated

CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
SQ Sequence 1813 BP; 506 A; 397 C; 439 G; 471 T;
Query Match 74.3%; Score 1538; DB 14; Length 1813;
Best Local Similarity 94.4%; Pred. No. 0.00e+00;
Matches 1682; Conservative 0; Mismatches 90; Indels 9; Gaps 4;
MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 01:26:17 1997; MasPar time 1317.77 Seconds
Tabular output not generated.
Title: >US-08-436-265-13
Description: (1-2070) from US08436265.seq
Perfect Score: 2070
N.A. Sequence: 1 ATTCATGAGATGGAGCATATA.....TTTGCTTTTTTTGTTTGT 2070
Comp: TAAGTACTCTACCTTCGTAT.....AAACGAAAAAACAACAA
Scoring table:
TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 887282 seqs, 320523884 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: EST-STS
SUMMARIES
Result Query
No. Score Match Length DB ID Description Pred. No.
1 328 15.8 404 165 W39552 zc18g04.r1 Soares par 0.00e+00
2 237 11.4 285 93 MWTEST730 M.musculus expressed 0.00e+00
3 231 11.2 259 38 H33315 EST109182 Rattus sp. 0.00e+00
4 208 10.0 263 116 N88732 K5301F Fetal heart, L 0.00e+00
5 142 6.9 471 164 W34981 mc33h08.r1 Soares mou 5.03e-223
6 141 6.8 739 10 AA053838 zf53c07.r1 Soares ret 5.78e-221
7 141 6.8 739 231 HSA53838 zf53c07.r1 Soares ret 5.78e-221
8 104 5.0 515 43 C17679 Human placenta cDNA 5 8.01e-146
9 104 5.0 515 239 HSC6799 Human placenta cDNA 5 8.01e-146
10 100 4.8 357 65 HSC22A061 H. sapiens partial cD 7.28e-138
11 96 4.6 211 61 HSC0HE101 H. sapiens partial cD 6.02e-130
MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sat May 24 07:06:02 1997; MasPar time 70.46 Seconds
Tabular output not generated.
Title: >US-08-436-265-13
Description: (1-2070) from US08436265.seq
Perfect Score: 2070
N.A. Sequence: 1 ATTCATGAGATGGAGCATATA.....TTTGCTTTTTTTGTTTGT 2070
Comp: TAAGTACTCTACCTTCGTAT.....AAACGAAAAAACAACAA
Scoring table:
TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 53119 seqs, 14293498 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:51 2:52 3:53 4:54 5:55 6:PT90 7:PT91 8:PT92 9:PT93
10:PT94 11:PT95 12:PT96
Statistics: Mean 9.280; Variance 5.006; scale 1.854
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1538	74.3	1813	10	PCT-US94-1	Sequence 1, Applicatio	0.00e+00
2	1417	68.5	2932	11	PCT-US95-0	Sequence 5, Applicatio	0.00e+00
3	520	25.1	1952	11	PCT-US95-0	Sequence 7, Applicatio	0.00e+00
4	516	24.9	2076	10	PCT-US94-1	Sequence 3, Applicatio	0.00e+00
5	259	12.5	1794	10	PCT-US94-1	Sequence 9, Applicatio	2.46e-174
6	252	12.2	1506	5	US-08-317-	Sequence 4, Applicatio	6.84e-169
7	252	12.2	1506	5	US-08-149-	Sequence 4, Applicatio	6.84e-169
8	253	12.2	1647	10	PCT-US94-1	Sequence 7, Applicatio	1.14e-169
9	243	11.7	1506	5	US-08-149-	Sequence 2, Applicatio	6.70e-162
10	243	11.7	1506	5	US-08-317-	Sequence 2, Applicatio	6.70e-162

ALIGNMENTS
RESULT 1
ID PCT-US94-10080-1 STANDARD; DNA; UNC; 1813 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9410080.
CC Sequence 1, Application PC/TUS9410080
CC GENERAL INFORMATION:
CC APPLICANT: GENETICS INSTITUTE, INC.
CC TITLE OF INVENTION: RECEPTOR PROTEINS
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
Query Match 74.3%; Score 1538; DB 10; Length 1813;
Best Local Similarity 94.4%; Pred. No. 0.00e+00;
Matches 1682; Conservative 0; Mismatches 90; Indels 9; Gaps 4;
RESULT 2
ID PCT-US95-05467-5 STANDARD; DNA; UNC; 2932 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 5, Application PC/TUS9505467.
CC Sequence 5, Application PC/TUS9505467
CC GENERAL INFORMATION:
CC APPLICANT:
CC APPLICANT:
CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL
CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jun 24 17:53:39 1997; MasPar time 11.06 Seconds
524.120 Million cell updates/sec
Tabular output not generated.
Title: >US-08-436-265-14
Description: (1-532) from US08436265.pep
Perfect Score: 3986
Sequence: 1 MTQLYTYIRLLGACLFIIH.....TALRIKTKTLAKMVESQDVKI 532
Scoring table: PAM 150
Gap 11

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-genesed26

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 36.022; Variance 149.415; scale 0.241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3986	100.0	532 19	R95225	Mouse BMP type I rece	0.00e+00
2	3986	100.0	532 17	R96201	Bone morphogenetic pr	0.00e+00
3	3986	100.0	532 13	R74343	BRK-1 protein.	0.00e+00
4	3961	99.4	532 13	R70237	Bone morphogenic prot	0.00e+06
5	3915	98.2	532 14	R85207	Human ALK-3.	0.00e+00
6	3915	98.2	532 10	R55368	Human Activin recepto	0.00e+00
7	3686	92.5	500 13	R74342	Truncated BRK-1.	0.00e+00
8	2756	69.1	502 14	R85206	Mouse ALK-6.	6.06e-267
9	2756	69.1	502 13	R70238	Bone morphogenic prot	6.06e-267
10	2746	68.9	502 19	R95226	Chick BMP type I rece	6.56e-266

ALIGNMENTS

RESULT 1
ID R95225 standard; Protein; 532 AA.
AC R95225;
DT 31-DEC-1996 (first entry)
DE Mouse BMP type I receptor kinase protein (BRK-1).
KW BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
KW BMP type I receptor kinase; BRK-1; BMP receptor.
OS Mus sp.
PN W09614579-A1.
PD 17-MAY-1996.
PF 30-OCT-1995; U14027.
PR 04-NOV-1994; US-334178.
PR 05-JUN-1995; US-462467.
PR (PROC) PROCTER & GAMBLE CO.
PI Rosenbaum JS;
DR WPI; 96-251887/25.
DR N-PSDB; T95225.
PT Assays for bone morphogenetic protein activities - using complex of
PT BMP type I receptor kinase protein and BMP receptor kinase protein
PT BRK-3
PS Claim 2; Page 66-67; 101pp; English.
CC Full-length mouse bone morphogenetic protein (BMP) type I receptor
CC kinase protein-1 (BRK-1) (R95225) is a receptor capable of binding
CC BMP and transducing a signal initiated by the binding. Its amino
CC acid sequence was deduced from a cDNA clone (T28021). A BMP
CC receptor kinase protein complex formed of full-length, incomplete
CC or soluble BMP type I receptor kinase protein and full-length,
CC incomplete or soluble BMP type II receptor kinase-3 (BRK-3) (see
CC also R95222-24 and R95226-34) is useful for screening cpds. for BMP
CC receptor affinity or for determining the concentration of a BMP
CC receptor ligand in a clinical sample. The complex can be expressed
CC by host cells co-transfected with vectors carrying the appropriate
CC DNA sequences (see also T28018-30).
SQ Sequence 532 AA;

Query Match 100.0%; Score 3986; DB 19; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

ID R96201 standard; Protein; 532 AA.
AC R96201;
DT 22-AUG-1996 (first entry)
DE Bone morphogenetic protein type-I receptor kinase-1.
KW Mouse; bone morphogenetic protein receptor kinase-1;
KW bone morphogenetic protein receptor kinase-3; antibody; diagnostic;
KW bone disorder; osteogenic; bone morphogenetic protein-agonist;
KW drug screening; reporter gene; bone morphogenetic protein-antagonist;
KW hormone-responsive element.
OS Mus musculus.
FH Key Location/Qualifiers
FT Peptide 216..221
FT /note= "Conserved BRK-1 motif"
FT Peptide 398..421
FT /note= "Peptide used to raise antibody"
PN W09614412-A2.
PD 17-MAY-1996.
PF 30-OCT-1995; U14085.
PR 04-NOV-1994; US-334179.
PA (PROC) PROCTER & GAMBLE CO.
PI Nohn T, Rosenbaum JS;

RESULT 3

ID R74343 standard; Protein; 532 AA.
AC R74343;
DT 01-NOV-1995 (first entry)
DE BRK-1 protein.
KW BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein.
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide
FT Domain 24..152
FT /label= Extracellular_ligand_binding_domain
FT Domain 153..176
FT /label= Transmembrane_domain
FT Domain 177..532
FT /label= Intracellular_kinase_domain
PN W09514778-A.
PD 01-JUN-1995.
PF 23-NOV-1994; U13534.
PR 24-NOV-1993; US-158735.
PA (PROC) PROCTER & GAMBLE CO.
PI Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;
DR WPI; 95-206935/27.
DR N-PSDB; Q90184.

PT New bone morphogenetic protein receptor kinase protein - used for
PT identifying cpds. capable of binding it and for developing therapeutic
PT cpds. and detection system(s)
PS Claim 1; Page 29-32; 49pp; English.
CC A cDNA library prepared from NIH3T3 poly-A RNA was screened with
CC J159 PCR fragment to isolate clone BRK-1 (sequence given in
CC Q90184) encoding full-length BMP receptor kinase protein (R74343).
CC Vectors including the DNA were used to express recombinant BRK-1 in
CC CHO and COS-7 hosts.
SQ Sequence 532 AA;

Query Match 100.0%; Score 3986; DB 13; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

ID R70237 standard; Protein; 532 AA.
AC R70237;
DT 28-SEP-1995 (first entry)
DE Bone morphogenic protein receptor CFK1-23a.
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;

KW bone, cartilage; injury; treatment; inhibition.
OS Rattus rattus.
PN WO9507982-A.
PF 23-MAR-1995.
PR 07-SEP-1994; U10080.
PR 17-SEP-1993; US-123934.
PA (GEM) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
DR N-PSDB; Q83530.
PT Truncated BMP and serine/threonine kinase receptor proteins -
PT used to inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 16; Page 50-51; 83pp; English.
CC Truncated bone morphogenic protein (BMP) receptors and
CC serine/threonine kinase receptors may be used in compositions to
CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
CC receptors pref. comprise the ligand binding domain, but not the
CC serine/threonine kinase and transmembrane domains. The truncated
CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
CC Sequence 532 AA;

Query Match 99.4%; Score 3961; DB 13; Length 532;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mtqlytyrllgacflfiishvqgnldsmhgtgmksdvdqkpgenvtlapedtlpflk 60
QY 1 MTQLTYTYRLLGACFLFIISHVQGNLD SMLHGTGMKSDLDQKRPENGVTLPEDTLPFLK 60

Db 61 cycsgchpcddainntcithgchfaieeddqgettlsgcmkyegsdqckdspkaqlrr 120
QY 61 CYCSGCHPCDDAINNTCITHGCHFAIEEDDQGETTLTSGCMKYEGSDQCKDSPKAQLRR 120

Db 121 tieccrtnlcngylqptlpvpgffdgsvrwlavlismavciavmifscfcykhy 180
QY 121 TIECCRTNLCNGYLQPTLPVPGFFDGSI RVLVLSMAVCIVAMIFSCFCYKHYC 180

Db 181 ksissrgyrnrldqgeafipvgeslkdldsgsgsgsglpllvqrtaikqimvrq 240
QY 181 KSISSRGRYNRDLEQDEAFIPVGESLKDLDQSGSGSGGLPLLVQRTIAKIQMVRQV 240

Db 241 gkgrgyevwmkgwrgkvavkvfftteaswfreteiyqvtlrmhenilgfaadikgtg 300
QY 241 GKGRGYEVWMKGWKGKAVKVFFTTEASWFRTEIYQVTLRMHENILGFAADIKGTG 300

Db 301 swtqllyitdyhengsllydfkcatldtrallklaysaacglchlhteiygtqgkpaiah 360
QY 301 SWTQLYLIITDYHENGSLYDFLKCATLDRALLKLAISAACGLCHLHTEIYGTQGPAAIAH 360

Db 361 rdlkskniliikkngscctiadlgavkfnsdtnedvplntrvgrtrrymapevldeslkn 420
QY 361 RDLKSKNILLIKKNGSCCTIADLGAVKFNSDTNEVDIPLNTRVGRTRRYMAPEVLDES LNKN 420

Db 421 hfqpyimadiysfgliiwemarrcitggiveeyqlpynmvpdspsyedmrevvcvkrllr 480
QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPDSPSYEDMREVVCVKRLR 480

Db 481 pivsnrwnsdeclravlkmlsecwahnpsarlalrikktlakmvesqdsvki 532
QY 481 PIVSNRWNSENCLRAVLKLMSECAHNPASRLALRIKKTAKMVESQDVKI 532

RESULT 5
ID R85207 standard; Protein; 532 AA.
AC R85207;
DT 13-FEB-1996 (first entry)
DE Human ALK-3.

KW ALK-3; OPI binding receptor; osteogenic protein 1; morphogenesis;
KW morphogen; agonist; antagonist.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide
FT Domain 24..152
FT /label= Extracellular_domain
FT Domain 153..235
FT /label= Transmembrane_domain
FT Domain 236..527
FT /label= Intracellular_domain
FT /note= "serine/threonine-kinase domain"
PN WO9530003-A2.
PD 09-NOV-1995.
PF 28-APR-1995; U05467.
PR 29-APR-1994; US-236428.
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (LUDW-) LUDWIG INST CANCER RES.
PI DiJke PT, Heldin C, Miyazano K, Sampath KT;
DR WPI; 95-393076/50.
DR N-PSDB; T06031.
PT Identifying osteogenic protein-1 receptor-binding analogue - useful
PT in the design of morphogen agonists and antagonists for therapeutic,
PT diagnostic and experimental purposes
PS Claim 1; Page 68-71; 95pp; English.
CC The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (given in
CC R85206, R85207 and R85209) have specific binding affinity for
CC osteogenic protein 1 (OP1) and OPI-related analogues. The
CC receptors are used to identify novel morphogen receptor binding
CC analogues useful in drug design.
SQ Sequence 532 AA;

Query Match 98.2%; Score 3915; DB 14; Length 532;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 522; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 1 mtqlytyrllgacflfiishvqgnldsmhgtgmksdvdqkpgenvtlapedtlpflk 60
QY 1 MTQLTYTYRLLGACFLFIISHVQGNLD SMLHGTGMKSDLDQKRPENGVTLPEDTLPFLK 60

Db 61 cycsgchpcddainntcithgchfaieeddqgettlsgcmkyegsdqckdspkaqlrr 120
QY 61 CYCSGCHPCDDAINNTCITHGCHFAIEEDDQGETTLTSGCMKYEGSDQCKDSPKAQLRR 120

Db 121 tieccrtnlcngylqptlpvpgffdgsvrwlavlismavciavmifscfcykhy 180
QY 121 TIECCRTNLCNGYLQPTLPVPGFFDGSI RVLVLSMAVCIVAMIFSCFCYKHYC 180

Db 181 ksissrryrnrldqgeafipvgeslkdldsgsgsgsglpllvqrtaikqimvrq 240
QY 181 KSISSRGRYNRDLEQDEAFIPVGESLKDLDQSGSGSGGLPLLVQRTIAKIQMVRQV 240

Db 241 gkgrgyevwmkgwrgkvavkvfftteaswfreteiyqvtlrmhenilgfaadikgtg 300
QY 241 GKGRGYEVWMKGWKGKAVKVFFTTEASWFRTEIYQVTLRMHENILGFAADIKGTG 300

Db 301 swtqllyitdyhengsllydfkcatldtrallklaysaacglchlhteiygtqgkpaiah 360
QY 301 SWTQLYLIITDYHENGSLYDFLKCATLDRALLKLAISAACGLCHLHTEIYGTQGPAAIAH 360

Db 361 rdlkskniliikkngscctiadlgavkfnsdtnedvplntrvgrtrrymapevldeslkn 420
QY 361 RDLKSKNILLIKKNGSCCTIADLGAVKFNSDTNEVDIPLNTRVGRTRRYMAPEVLDES LNKN 420

Db 421 hfqpyimadiysfgliiwemarrcitggiveeyqlpynmvpdspsyedmrevvcvkrllr 480
QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPDSPSYEDMREVVCVKRLR 480
Db 481 pivsnrwnsdeclravlkmlsecwahnpsarlalrikktlakmvesqdsvki 532

Qy 481 PIVSNRNSDECLRAVLKLMSECAHNPASRUTALRIKKTAKWVESQDVKI 532

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jun 24 17:52:10 1997; MasPar time 19.41 Seconds

781.251 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-14
Description: (1-532) from US08436265.pep
Perfect Score: 3986
Sequence: 1 MTQLYTYRLLGLACLFIIISH.....TALRIKKTAKWVESQDVKI 532

Scoring table: PAM 150
Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann16:unrev

Statistics: Mean 48.972; Variance 115.254; scale 0.425

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	3986	100.0	532	14	A56238 bone morphogenetic p	0.00e+00
2	3961	99.4	532	14	JC2387 bone morphogenetic p	0.00e+00
3	3915	98.2	532	13	S37183 ALK-3 protein - huma	0.00e+00
4	3915	98.2	532	13	I37163 ALK-3 - human	0.00e+00
5	3686	92.5	500	14	A56238 bone morphogenetic p	0.00e+00
6	3124	78.4	527	12	A54985 BMP receptor precurs	0.00e+00
7	2756	69.1	502	14	A53444 activin receptor-lik	0.00e+00
8	2756	69.1	502	14	JC2491 serine/threonine kin	0.00e+00
9	2746	68.9	502	13	A56683 receptor protein kin	0.00e+00
10	1770	44.4	503	13	A49432 activin receptor-lik	1.52e-283
11	1763	44.2	503	14	JC2061 transforming growth	2.75e-282

ALIGNMENTS

```
RESULT 1
ENTRY JC2387 #type complete
TITLE bone morphogenetic protein receptor BRK-1 - mouse
ALTERNATE_NAMES ALK-3 protein; BMP receptor
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 06-Sep-1996
ACCESSIONS A56238; S40158; I48242; I49543
REFERENCE A56238
#authors Koenig, B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman, J.P.; Correa, P.E.; Olson, C.A.; Pecquet, A.L.; Ventura, F.; Grant, R.A.; Chen, G.X.; Wrana, J.L.; Massague, J.; Rosenbaum, J.S.
#journal Mol. Cell. Biol. (1994) 14:5961-5974
#title Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cells.
#accession A56238
##status preliminary
##molecule_type mRNA
##residues 1-532 #label KOE
##cross-references GB:U04672
```

```
REFERENCE S40158
#authors Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
#submission submitted to the EMBL Data Library, June 1993
#description ALK-3 and ALK-6: the closely related members in the serine/threonine kinase receptor family.
#accession S40158
##status preliminary
##molecule_type mRNA
##residues 1-532 #label MIY
##cross-references EMBL:223154
REFERENCE I48241
#authors Dewulf, N.; Verschueren, K.; Lonnay, O.; Moren, A.; Grimsby, S.; Vande Spiegle, K.; Miyazono, K.; Huylebroeck, D.; Ten Dijke, P.
#journal Endocrinology (1995) 136:2652-2663
#title Distinct spatial and temporal expression patterns of two type I receptors for bone morphogenetic proteins during mouse embryogenesis.
#cross-references MUID:95269711
#accession I48242
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-532 #label RES
##cross-references EMBL:223154; NID:g437868; CDS_PID:g437869
REFERENCE I49543
#authors Suzuki, A.; Tilles, R.S.; Yamaji, N.; Song, J.J.; Wozney, J.; Murakami, K.; Kung, H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:10255-10259
#title A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryo.
#cross-references MUID:95024052
#accession I49543
##status translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-532 #label RE2
##cross-references GB:D16250; NID:g577633; CDS_PID:g577634
CLASSIFICATION #superfamily protein kinase homology
KEYWORDS phosphotransferase; transmembrane protein
FEATURE 1-23 #domain signal sequence #status predicted #label SIG\
232-528 #domain protein kinase homology #label KIN
SUMMARY #length 532 #molecular-weight 60063 #checksum 6896
Query Match 100.0%; Score 3986; DB 14; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 2
ENTRY JC2387 #type complete
TITLE bone morphogenetic protein type IA receptor - rat
ALTERNATE_NAMES #formal_name Rattus norvegicus #common_name Norway rat
ORGANISM #formal_name Rattus norvegicus #sequence_revision 20-Feb-1995 #text_change 05-Jan-1996
DATE 05-Jan-1996
ACCESSIONS JC2387
REFERENCE JC2387
#authors Takeda, K.; Oida, S.; Ichijo, H.; Iimura, T.; Maruoka, Y.; Amagasa, T.; Sasaki, S.
#journal Biochem. Biophys. Res. Commun. (1994) 204:203-209
#title Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP.
#accession JC2387
##molecule_type mRNA
##residues 1-532 #label TAK
##cross-references DBJ:D38082
CLASSIFICATION #superfamily protein kinase homology
KEYWORDS glycoprotein; receptor; transmembrane protein
FEATURE 1-23 #domain signal sequence #status predicted #label SIG\
24-527 #product bone morphogenetic protein type IA receptor
```


153-175 #status predicted #label BMP\

232-528 #domain transmembrane #status predicted #label TMM\

236-527 #domain protein kinase homology #label KIN\

73 #region kinase domain\

#binding site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 532 #molecular-weight 59994 #checksum 7758

Query Match 99.4%; Score 3961; DB 14; Length 532;

Best Local Similarity 98.9%; Pred. No. 0.00e+00;

Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

RESULT 3

ENTRY S37183 #type complete

ENTRY ALK-3 protein - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Dec-1995

ACCESSIONS S37183

REFERENCE S37181

#authors ten Dijke, P.P.; Ichijo, H.H.; Franzen, P.P.; Schulz, P.P.; Saras, J.J.; Toyoshima, H.H.; Heldin, C.C.; Miyazono, K.K.

#submission submitted to the EMBL Data Library, April 1993

#description Activin receptor-like kinases; Anovel subclass of cell surface receptors with predicted serine/threonine kinase activity.

#accession S37183

#status preliminary

#molecule_type mRNA

#residues 1-532 #label TEN

#cross-references EMBL:222535

CLASSIFICATION #superfamily protein kinase homology

FEATURE

232-528 #domain protein kinase homology #label KIN

SUMMARY #length 532 #molecular-weight 60201 #checksum 6778

Query Match 98.2%; Score 3915; DB 13; Length 532;

Best Local Similarity 98.1%; Pred. No. 0.00e+00;

Matches 522; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

RESULT 5

ENTRY B56238 #type complete

ENTRY bone morphogenetic protein receptor BRK-1 (clone J159-7) - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995

ACCESSIONS B56238

REFERENCE A56238

#authors Koenig, B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman, J.P.; Correa, P.E.; Olson, C.A.; Pecquet, A.L.; Ventura, F.; Grant, R.A.; Chen, G.X.; Wrana, J.L.; Massague, J.; Rosenbaum, J.S.

#journal Mol. Cell. Biol. (1994) 14:5961-5974

#title Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cells.

#accession B56238

#status preliminary

#molecule_type mRNA

#residues 1-500 #label KOE

#cross-references GB:004673

#note neither protein nor nucleotide sequence is given; it is unclear whether this clone represents a naturally occurring variant or an incompletely processed mRNA transcript

SUMMARY #length 500 #molecular-weight 56438 #checksum 4304

Query Match 92.5%; Score 3686; DB 14; Length 500;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

ENTRY A54985 #type complete

ENTRY BMP receptor precursor - African clawed frog

ORGANISM #formal_name Xenopus laevis #common_name African clawed frog

DATE 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 08-Dec-1995

ACCESSIONS A54985

REFERENCE A54985

#authors Graff, J.M.; Thies, R.S.; Song, J.J.; Celeste, A.J.; Melton, D.A.

#journal Cell (1994) 79:169-179

#title Studies with a Xenopus BMP receptor suggest that ventral mesoderm-inducing signals override dorsal signals in vivo.

#accession A54985

#status preliminary; not compared with conceptual translation

#molecule_type mRNA

#residues 1-527 #label GRA

#note nucleotide sequence is not given

CLASSIFICATION #superfamily protein kinase homology

FEATURE

227-523 #domain protein kinase homology #label KIN

SUMMARY #length 527 #molecular-weight 59800 #checksum 7791

Query Match 78.4%; Score 3124; DB 12; Length 527;

Best Local Similarity 79.9%; Pred. No. 0.00e+00;

Matches 421; Conservative 5; Mismatches 45; Indels 6; Gaps 4;

Db 6 fiacfga-lllvhtqgqdfnlphrtgmksnspkqngvltapedlplfincvsgy 64

Qy 7 YIRLLGACLFIIISHVQGNLDMLHGTGMKSDLDQKRPENGVTLPEDTLPFLKCYCSGH 66

Db 65 cpqnavntcitngqcfamieejngdiiltsgcmkmeqsfqcdskpalsrrtieceor 124

Qy 67 CPDDAINTCITNGHCPAIEEDDQGETILTSGCMKYEGSDFOCKDSPAQLRRTIECCR 126

Db 125 tdfcnrdleptlskisdgey--alrfialliislvvclilivgfiliwiykhh--klhsq 180

Qy 127 TMLCNQYLQPTLPVPIGVFFPDGSRNLVVLISMAVCIVAMIIIFS-SCFCYKHYSISS 185

Db 181 rnlvnrldpddafipagesikalidissgsgsglpilvqvtiakiqmvrgiqgry 240

Qy 186 RGRYNRDLQDEAFIPVGESLKDLDQSSGSGSLPLVQRTIAKQIQMVYRQVGKGRY 245

Db 241 gevwmqkrgkvavkvfftaseawfretetiqtvlmrhenilgfiaadiktgswtqm 300

Qy 246 GEVWMQKRGKVAVKVFFTTTEEASWFRETEIQTVLMRHENILGFIAADIKTGSWTQL 305

Db 301 Yliteyhengslydflkcttdlrsllklaysaacglchlnhteivgtgkpaiahrdlks 360

Qy 306 YLITDYHENGSLYDFLKCATLDFTRALLKLAYSAAACGLCHLHTEIYGTGKPAIAHRDLKS 365

Db 361 knilikenwtcciadlglavkfnsdthvediplntrvgtkrymapevldeslnknfhqay 420

Qy 366 KNILIKNGSCCIIADLGLAVKFNSDINEVDIPLNTRVGTGRYMAPEVLDESINKHFPQY 425

Db 421 imadiysflliwemrrcitggiveeyqlpyymvmpndpsfmedrevvcmkclrtvsn 480

Qy 426 IMADIYSFGLIIEWEMARRCITGGIVEEYQLPYVMVMPDPSFEDMREVVCVRLRIVSN 485

Db 481 rwnsdeclravlkmaecwagpnasrltalrkktklkmvesqdski 527

Qy 486 RWNSECLRAVLKIMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532

RESULT 7

ENTRY A53444 #type complete

ENTRY activin receptor-like kinase 6 precursor - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 19-May-1994 #sequence_revision 19-May-1994 #text_change 08-Dec-1995

ACCESSIONS A53444; S40159

153-175 #status predicted #label BMP\

232-528 #domain transmembrane #status predicted #label TMM\

236-527 #domain protein kinase homology #label KIN\

73 #region kinase domain\

#binding site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 532 #molecular-weight 59994 #checksum 7758

Query Match 99.4%; Score 3961; DB 14; Length 532;

Best Local Similarity 98.9%; Pred. No. 0.00e+00;

Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

RESULT 3

ENTRY S37183 #type complete

ENTRY ALK-3 protein - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Dec-1995

ACCESSIONS S37183

REFERENCE S37181

#authors ten Dijke, P.P.; Ichijo, H.H.; Franzen, P.P.; Schulz, P.P.; Saras, J.J.; Toyoshima, H.H.; Heldin, C.C.; Miyazono, K.K.

#submission submitted to the EMBL Data Library, April 1993

#description Activin receptor-like kinases; Anovel subclass of cell surface receptors with predicted serine/threonine kinase activity.

#accession S37183

#status preliminary

#molecule_type mRNA

#residues 1-532 #label TEN

#cross-references EMBL:222535

CLASSIFICATION #superfamily protein kinase homology

FEATURE

232-528 #domain protein kinase homology #label KIN

SUMMARY #length 532 #molecular-weight 60201 #checksum 6778

Query Match 98.2%; Score 3915; DB 13; Length 532;

Best Local Similarity 98.1%; Pred. No. 0.00e+00;

Matches 522; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

RESULT 5

ENTRY B56238 #type complete

ENTRY bone morphogenetic protein receptor BRK-1 (clone J159-7) - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995

ACCESSIONS B56238

REFERENCE A56238

#authors Koenig, B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman, J.P.; Correa, P.E.; Olson, C.A.; Pecquet, A.L.; Ventura, F.; Grant, R.A.; Chen, G.X.; Wrana, J.L.; Massague, J.; Rosenbaum, J.S.

#journal Mol. Cell. Biol. (1994) 14:5961-5974

#title Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cells.

#accession B56238

#status preliminary

#molecule_type mRNA

#residues 1-500 #label KOE

#cross-references GB:004673

#note neither protein nor nucleotide sequence is given; it is unclear whether this clone represents a naturally occurring variant or an incompletely processed mRNA transcript

SUMMARY #length 500 #molecular-weight 56438 #checksum 4304

Query Match 92.5%; Score 3686; DB 14; Length 500;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE A53444
#authors ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho, M.; Miyazono, K.; Heldin, C.H.
#journal Science (1994) 264:101-104
#title Characterization of type I receptors for transforming growth factor-beta and activin.

#accession A53444
##status preliminary
##molecule_type mRNA
##residues 1-502 #label TEN
##cross-references GB:Z23143
REFERENCE S40158
#authors Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
#submission submitted to the EMBL Data Library, June 1993
#description ALK-3 and ALK-6: the closely related members in the serine/threonine kinase receptor family.

#accession S40159
##status preliminary
##molecule_type mRNA
##residues 1-502 #label MTY
##cross-references EMBL:Z23143
CLASSIFICATION #superfamily protein kinase homology
#domain protein kinase homology #label KIN
#length 502 #molecular_weight 56944 #checksum 5099

Query Match 69.1%; Score 2756; DB 14; Length 502;
Best Local Similarity 72.1%; Pred. No. 0.00e+00;
Matches 364; Conservative 76; Mismatches 60; Indels 5; Gaps 5;

MPsearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 14:34:01 1997; MasPar time 4.89 Seconds
Tubular output not generated.
358.195 Million cell updates/sec

Title: >US-08-436-265-14
Description: (1-532) from US08436265.pep
Perfect Score: 3986
Sequence: 1 MTQLYTYIRLLGACLFIIISH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: PAM 150
Gap 11

Searched: 35845 seqs, 3290575 residues

Processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:51 2:52 3:53 4:54 5:55 6:PT90 7:PT91 8:PT92 9:PT93
10:PT94 11:PT95 12:PT96

Statistics: Mean 33.997; Variance 162.888; scale 0.209

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	3961	99.4	PCT-US94-1 Sequence 2, Applicatio 0.00e+00
2	3915	98.2	PCT-US95-0 Sequence 6, Applicatio 0.00e+00
3	2756	69.1	PCT-US94-1 Sequence 4, Applicatio 4.94e-232
4	2756	69.1	PCT-US95-0 Sequence 8, Applicatio 4.94e-232
5	1763	44.2	PCT-US94-1 Sequence 10, Applicati 3.14e-143
6	1746	43.8	US-08-149- Sequence 17, Applicati 1.03e-141

Qy 89 DDQGETTLTSGCMKYEGSDPQCKDSRAQLRRRTIECCRT-NLCNQYLQPTLPPVVIGPFF 147
Db 120 DGPIHHKALLISVTVCSLLVLIL-FCYFRY-KROEARPRYSIGLEODETVIPGESLR 177
Qy 148 DGSIRWLVLISMAVCIVAMIISSSCFCYKHYCKSISSRGRYNPDLEQDEAFIPGESLK 207
Db 178 DLIEQSOSGGSGGLPLLQVORTIAQIQMWKOIGKGRYGEVMMGKWRGEKVAVKVFFTTT 237
Qy 208 DLIDQSOSGGSGGLPLLQVORTIAQIQVROVQKGRYGEVMMGKWRGEKVAVKVFFTTT 267
Db 238 EASWFRETEIQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLD 297
Qy 268 EASWFRETEIQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDFLKCATLD 327
Db 298 AKSMLKLAYSSVSGLCHLHTEIFSTQGRPAIAHROLKSKNLIKNGTCCIADLGLAVKF 357
Qy 328 TRALLKLAYSACGLCHLHTEIYGTQGRPAIAHROLDUKSNLIKNGSCCIIADLGLAVKF 387
Df 358 ISDTNEVDIPNTRVGTGKRYMPPPEVLDESINRTHI2SYIMADMYSFGLILWEIARRCVSG 417
Qy 388 NSDTNEVDIPLNTRVGTGKRYMAPEVLDESINRKNHFQPYIMADIYSFGLIIEWEMARRCITG 447
418 GIVEEYQLPYHDLVPSDPSEDNREIVCMKKLRPSPNRSWSSDECLRMGKLMTECAHN 477
448 GIVEEYQLPYNNVPSDPSEDNREIVCVKRI VSNRWNSECLRAVLKLMSECAHN 507
Db 478 PASRLTALRVKKTAKMSSESODIKL 502
Qy 508 PASRLTALRIKKTAKMVESQDVKI 532